



SEQUENCE LISTING

<110> Basi, Guriq
Saldanha, Jose
Yednock, Ted

<120> HUMANIZED ANTIBODIES THAT RECOGNIZE
BETA-AMYLOID PEPTIDE

<130> ELN-002

<140> US 10/010,942

<141> 2001-12-06

<150> US 60/251,892

<151> 2000-12-06

<160> 63

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 396

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(396)

<221> sig_peptide

<222> (1)...(60)

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gaa	acc	aac	ggt	tat	gtt	gtg	atg	acc	cag	act	cca	ctc	act	ttg	tgc	96
Glu	Thr	Asn	Gly	Tyr	Val	Val	Met	Thr	Gln	Thr	Pro	Leu	Thr	Leu	Ser	
			1				5						10			

gtt	acc	att	gga	caa	cca	gcc	tcc	atc	tct	tgc	aag	tca	agt	cag	agc	144
Val	Thr	Ile	Gly	Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	
		15				20					25					

ctc	tta	gat	agt	gat	gga	aag	aca	tat	ttg	aat	tgg	ttg	tta	cag	agg	192
Leu	Leu	Asp	Ser	Asp	Gly	Lys	Thr	Tyr	Leu	Asn	Trp	Leu	Leu	Gln	Arg	
	30				35					40						

cca	ggc	cag	tct	cca	aag	cgc	cta	atc	tat	ctg	gtg	tct	aaa	ctg	gac	240
Pro	Gly	Gln	Ser	Pro	Lys	Arg	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Asp	
45					50					55				60		

tct	gga	gtc	cct	gac	agg	ttc	act	ggc	agt	gga	tca	ggg	aca	gat	ttt	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
			65					70						75		

aca	ctg	aaa	atc	agc	aga	ata	gag	gct	gag	gat	ttg	gga	ctt	tat	tat	336
Thr	Leu	Lys	Ile	Ser	Arg	Ile	Glu	Ala	Glu	Asp	Leu	Gly	Leu	Tyr	Tyr	
			80				85						90			

COPY OF PAPERS
ORIGINALLY FILED

tgc tgg caa ggt aca cat ttt cct cgg acg ttc ggt gga ggc acc aag 384
 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
 95 100 105

ctg gaa atc aaa 396
 Leu Glu Ile Lys
 110

<210> 2
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 <213> Mus musculus

<220>
 <221> SIGNAL
 <222> (1)...(20)

<400> 2
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 1 5 10
 Val Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
 15 20 25
 Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg
 30 35 40
 Pro Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Ile Glu Ala Glu Asp Leu Gly Leu Tyr Tyr
 80 85 90
 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gly Gly Thr Lys
 95 100 105
 Leu Glu Ile Lys
 110

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<220>
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 <222> (1)...(414)

<221> sig_peptide
 <222> (1)...(57)

<400> 3
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 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 -15 -10 -5

gtc cag tgt gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag 96
 Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
 1 5 10

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cct gga gcg tct ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc 144
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                20                25

agt aac tat ggc atg tct tgg gtt cgc cag aat tca gac aag agg ctg 192
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
    30                35                40                45

gag tgg gtt gca tcc att agg agt ggt ggt ggt aga acc tac tat tca 240
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                55                60

gac aat gta aag ggc cga ttc acc atc tcc aga gag aat gcc aag aac 288
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
                65                70                75

acc ctg tac ctg caa atg agt agt ctg aag tct gag gac acg gcc ttg 336
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
                80                85                90

tat tat tgt gtc aga tat gat cac tat agt ggt agc tcc gac tac tgg 384
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
    95                100                105

ggc cag ggc acc act gtc aca gtc tcc tca 414
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110                115

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<210> 4
<211> 138
<212> PRT
<213> Mus musculus

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<220>
<221> SIGNAL
<222> (1)...(19)

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<400> 4
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
          -15                -10                -5
Val Gln Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys
          1                5                10
Pro Gly Ala Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                20                25
Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Asn Ser Asp Lys Arg Leu
    30                35                40                45
Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Gly Arg Thr Tyr Tyr Ser
                50                55                60
Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala Lys Asn
    65                70                75
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu
    80                85                90
Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
    95                100                105
Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110                115

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<210> 5
 <211> 132
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 5
 Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
 -20 -15 -10 -5
 Glu Thr Asn Gly Tyr Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
 1 5 10
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
 15 20 25
 Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 Val Glu Ile Lys
 110

<210> 6
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> (1)...(13)

<400> 6
 Met Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
 -10 -5 1
 Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
 5 10 15
 Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
 20 25 30 35
 Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
 40 45 50
 Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
 55 60 65
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 70 75 80
 Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
 85 90 95
 Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 7
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 7
 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
 20 25 30
 Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
 85 90 95
 Leu Gln Thr Pro
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<210> 8
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 3D6 heavy chain variable region

<221> SIGNAL
 <222> (1)...(19)

<400> 8
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 -15 -10 -5
 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Arg Thr Tyr Tyr Ser
 50 55 60
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 65 70 75
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu
 80 85 90
 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
 95 100 105
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 110 115

<210> 9
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 9

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20           25           30
Ala Val Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
          85           90           95
Ala Lys Asp Asn Tyr Asp Phe Trp Ser Gly Thr Phe Asp Tyr Trp Gly
          100          105          110
Gln Gly Thr Leu Val Thr Val Ser Ser
          115          120

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<210> 10

<211> 98

<212> PRT

<213> Homo sapiens

<400> 10

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
          20           25           30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
          50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          85           90           95
Ala Lys

```

<210> 11

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<221> SIGNAL

<222> (1)...(20)

<223> humanized 3D6 light chain variable region

<400> 11

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Met Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg
-20           -15           -10           -5
Glu Thr Asn Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
          1           5           10
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser
          15           20           25
Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Lys
          30           35           40

```

Pro Gly Gln Ser Pro Gln Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Trp Gln Gly Thr His Phe Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 Val Glu Ile Lys
 110

<210> 12
 <211> 138
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Humanized 3D6 light chain variable region

<221> SIGNAL
 <222> (1)...(19)

<400> 12
 Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Val Leu Val Leu Lys Gly
 -15 -10 -5
 Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
 1 5 10
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 15 20 25
 Ser Asn Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 30 35 40 45
 Glu Trp Val Ala Ser Ile Arg Ser Gly Gly Arg Thr Tyr Tyr Ser
 50 55 60
 Asp Asn Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 65 70 75
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 80 85 90
 Tyr Tyr Cys Val Arg Tyr Asp His Tyr Ser Gly Ser Ser Asp Tyr Trp
 95 100 105
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 110 115

<210> 13
 <211> 393
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(393)

<221> sig_peptide
 <222> (1)...(57)

<400> 13
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 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
 -15 -10 -5

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tcc agc agt gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc 96
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
      1                      5                      10

agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag aac att 144
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
      15                      20                      25

ata cat agt aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca 192
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
      30                      35                      40                      45

ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
      50                      55                      60

ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca 288
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
      65                      70                      75

ctc aag atc aag aaa gtg gag gct gag gat ctg gga att tat tac tgc 336
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
      80                      85                      90

ttt caa ggt tca cat gtt ccg ctc acg ttc ggt gct ggg acc aag ctg 384
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
      95                      100                      105

gag ctg gaa 393
Glu Leu Glu
110

```

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<210> 14
<211> 131
<212> PRT
<213> Mus musculus

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<220>
<221> SIGNAL
<222> (1)...(19)

```

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<400> 14
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
      -15                      -10                      -5
Ser Ser Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val
      1                      5                      10
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile
      15                      20                      25
Ile His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
      30                      35                      40                      45
Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser
      50                      55                      60
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
      65                      70                      75
Leu Lys Ile Lys Lys Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys
      80                      85                      90
Phe Gln Gly Ser His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
      95                      100                      105
Glu Leu Glu
110

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<210> 15
 <211> 426
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(426)

<221> sig_peptide
 <222> (1)...(57)

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 Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
 -15 -10 -5

gtc ctg tcc cag gct act ctg aaa gag tct ggc cct gga ata ttg cag 96
 Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
 1 5 10

tcc tcc cag acc ctc agt ctg act tgt tct ttc tct ggg ttt tca ctg 144
 Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
 15 20 25

agc act tct ggt atg gga gtg agc tgg att cgt cag cct tca gga aag 192
 Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
 30 35 40 45

ggt ctg gag tgg ctg gca cac att tac tgg gat gat gac aag cgc tat 240
 Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
 50 55 60

aac cca tcc ctg aag agc cgg ctc aca atc tcc aag gat acc tcc aga 288
 Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
 65 70 75

aag cag gta ttc ctc aag atc acc agt gtg gac cct gca gat act gcc 336
 Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
 80 85 90

aca tac tac tgt gtt cga agg ccc att act ccg gta cta gtc gat gct 384
 Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
 95 100 105

atg gac tac tgg ggt caa gga acc tca gtc acc gtc tcc tca 426
 Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 110 115 120

<210> 16
 <211> 142
 <212> PRT
 <213> Mus musculus

<220>
 <221> SIGNAL
 <222> (1)...(19)

<400> 16

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Met Asp Arg Leu Thr Ser Ser Phe Leu Leu Leu Ile Val Pro Ala Tyr
      -15                      -10                      -5
Val Leu Ser Gln Ala Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
      1                      5                      10
Ser Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu
      15                      20                      25
Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys
      30                      35                      40                      45
Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr
      50                      55                      60
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg
      65                      70                      75
Lys Gln Val Phe Leu Lys Ile Thr Ser Val Asp Pro Ala Asp Thr Ala
      80                      85                      90
Thr Tyr Tyr Cys Val Arg Arg Pro Ile Thr Pro Val Leu Val Asp Ala
      95                      100                      105
Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
      110                      115                      120

```

<210> 17

<211> 136

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 17

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tccgcaagct tggccgacc atggacatgc gcggtgccgc ccagctgctg ggctgtgta 60
tgctgtgggt gtccggctcc tccggctacg tggatgatgac ccagtcctcc ctgtccctgc 120
ccgtgacccc cgcgca                                     136

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<210> 18

<211> 131

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 18

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ctgggggggac tggccgggct tctgcagcag ccagttcagg taggtcttgc cgtcggagtc 60
cagcaggggac tgggaggact tgcaggagat ggaggcgggc tcgccggggg tcacgggcag 120
ggacaggggg g                                           131

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<210> 19

<211> 146

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 19

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acctgaactg gctgctgcag aagcccggcc agtcccccca ggcctgatac tacctgggtg 60
ccaagctgga ctccggcgtg cccgaccgct tctccggctc cggctccggc accgacttca 120
ccctgaagat ctcccgctg gaggcc                                     146

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<210> 20
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
aattctagga tccactcacg cttgatctcc accttggtgc cctggccgaa ggtgcggggg 60
aagtgggtgc cctgccagca gtagtacacg cccacgtcct cggcctccac gcgggagatc 120
ttcagggtga agtcggtgcc gg 142

<210> 21
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 21
ctgggggggac tggccg 16

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 22
acctgaactg gctgctgcag aa 22

<210> 23
<211> 138
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 23
acagaaagct tgccgccacc atggagtttg ggctgagctg gctttttctt gtggctatatt 60
taaaagggtgt ccagtgtgag gtgcagctgc tggagtccgg cggcggcctg gtgcagcccg 120
gcggctccct gcgcctgt 138

<210> 24
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 24
gccgcgggag cggatggagg ccacccactc caggcccttg ccgggggcct ggcgcaccca 60
ggacatgccg tagttggaga aggtgaagcc ggaggcggcg caggacaggc gcaggagacc 120
gccgggctgc accag 135

<210> 25
<211> 142
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 25
ctggagtggg tggcctccat ccgctccggc ggcggccgca cctactactc cgacaacgtg 60
aaggggccgct tcaccatctc ccgcgacaac gcccaagaact ccctgtacct gcagatgaac 120
tccctgcgcg ccgaggacac cg 142

<210> 26
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 26
ctgcaaggat ccactcaccg gaggacacgg tcaccagggt gccctggccc cagtagtcgg 60
aggagccgga gtagtggtcg tagcgcacgc agtagtacag ggcggtgtcc tcggcgcgca 120
gggagttcat ctgcaggtac aggg 144

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27
gccgcccggag cggatg 16

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 28
ctggagtggg tggcctccat 20

<210> 29
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29
tccgcaagct tgccgccac 19

<210> 30
<211> 29

<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
aattcttagga tccactcacg ctgatctc

29

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 31
acagaaagct tgccgccacc atg

23

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 32
ctgcaaggat ccactcacg ga

22

<210> 33
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> native ABeta peptide

<400> 33
Asp Ala Glu Phe Arg His Asp Ser Gly Tyr
1 5 10

<210> 34
<211> 402
<212> DNA
<213> Artificial Sequence

<220>
<223> h3D6 version 1 VL

<400> 34
atggacatgc gcgtgccgc ccagctgctg ggccctgctga tgctgtgggt gtccggctcc 60
tccggctacg tggatgac ccagtcctgc ctgtccctgc ccgtgaccc cggcgagccc 120
gcctccatct cctgcaagtc ctccagctcc ctgctggact ccgacggcaa gacctacctg 180
aactggctgc tgcagaagcc cggccagctc cccagcgcc tgatctacct ggtgtccaag 240
ctggactccg gcgtgccga ccgttctcc ggctccggct ccggcaccga cttcaccctg 300
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 gctccatct cctgcaagtc ctcccagtc ctgtggact ccgacggcaa gacctacctg 180
 aactggctgc tgcagaagcc cggccagtc ccccagcgcc tgatctacct ggtgtccaag 240
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 ggcaagggcc tggagtgggt ggctccatc cgctccggcg gcggccgcac ctactactcc 240
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 cagatgaact ccctgcgcgc cgaggacacc gccctgtact actgctgctg ctacgaccac 360
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 tgcgccgct ccggcttcac cttctccaac tacggcatgt cctgggtgcg ccaggccccc 180
 ggcaagggcc tggagtgggt ggctccatc cgctccggcg gcggccgcac ctactactcc 240
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 cagatgaact ccctgcgcgc cgaggacacc gccctgtact actgctgctg ctacgaccac 360
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 <212> PRT
 <213> Homo sapiens

<400> 38
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 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
 20 25 30

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Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp	50	55	60
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu	65	70	75
Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn	85	90	95
Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val	100	105	110
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu	115	120	125
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys	130	135	140
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu	145	150	155
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile	165	170	175
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu	180	185	190
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	195	200	205
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys	210	215	220
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	225	230	235
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	245	250	255
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile	260	265	270
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg	275	280	285
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile	290	295	300
Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe	305	310	315
Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr	325	330	335
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr	340	345	350
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala	355	360	365
Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	370	375	380
Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala	385	390	395
Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	405	410	415
Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	420	425	430
Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	435	440	445
Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	450	455	460
Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	465	470	475
Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	485	490	495
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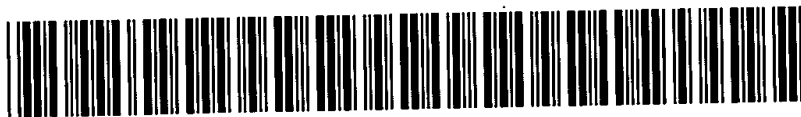
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Creation date: 12-15-2003
Indexing Officer: HKEFLAI - HELEN KEFLAI
Team: OIPEBackFileIndexing
Dossier: 10010942

Legal Date: 07-24-2002

No.	Docode	Number of pages
1	CRFL	1

Total number of pages: 1

Remarks:

Order of re-scan issued on